Remarks/Arguments

Claim 32 is allowed, claims 2 and 34 are objected to and claims 1, 4-8, 10, 11 and 13-15 are rejected. New claim 35 has been added. Claims 1, 4-8, 10-11, 13-15, 32 and 35 are pending. In the present response, claim 1 has been amended, claims 2 and 34 have been canceled without prejudice or disclaimer and new claim 35 has been added. Support for amended claim 1 can be found in the previously presented claims 2 and 34. Support for newly added claim 35 can be found in claims 32, 34 and throughout the specification.

Applicants have revised the paragraph beginning on line 22, page 4 of the specification to show that the genbank numbers for human and mouse dab1 are mRNAs instead of genes.

No new matter has been added by way of these amendments to the claims and specification. Reconsideration and withdrawal of the rejections are respectfully requested in light of these amendments and the following remarks.

In paragraph 4 of the Office Action dated February 21, 2006, the Examiner states that Applicants failed to provide an amendment directing entry of the paper copy of the sequence listing into the specification. Applicants respectfully disagree. On page 6 of Applicant's response dated November 21, 2005, the first sentence of the second paragraph states: "In place of the canceled sequence listing, Applicants request that the paper copy of the sequence listing filed herein be entered into the specification." However, to further prosecution, Applicants have provided an amendment to the sequence listing found on page 5 of this response.

Specification/Informalities

The Examiner pointed out that the paragraph beginning on line 22, page 4 of the specification contains new matter. Applicants apologize for this error and have revised this paragraph to replace dab1 "gene" with "mRNA".

35 U.S.C § 112, Second Paragraph

Claims 1, 4-8, 10-11 and 13-15 are rejected under 35 USC 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject

matter which Applicants regards as the invention. The Examiner asserts that the recitation of "a serine corresponding to position 491 of the polypeptide encoded by SEQ ID NO:4 and a serine corresponding to position 515 of the polypeptide encoded by SEQ ID NO:4" as it relates to a Dab1 comprising SEQ ID NO:3 is confusing and asks Applicants to clarify the meaning of the claim. The Examiner asserts that it is unclear as to which serine of a dab1 comprising SEQ ID NO:3 is intended as "corresponding to" position 491 or 515 of the polypeptide encoded by SEQ ID NO:4. The Examiner states that in accordance with MPEP 2111, the Examiner has interpreted the term "a serine corresponding to position 491 of the polypeptide encoded by SEQ ID NO:4 and a serine corresponding to position 515 of the polypeptide encoded by SEQ ID NO:4" as meaning any serine with a Dab1 polypeptide comprising SEQ ID NO:3. The Examiner asks that Applicants clarify the meaning of the term.

Applicants continue to assert that Dab1 proteins can easily be distinguished by a person of skill in the art and that structural references are not needed to identify a Dab1 protein. However, Applicants revised claim 1 so that if a Dab1 protein does not comprise the 14 amino acid sequence of SEQ ID NO:3, then that protein would lie outside the scope of the claim. Attached as Exhibit 1 is a list of proteins that contain conserved domains when compared to the Dab1 protein encoded by genbank no. 1771282 (SEQ ID NO:4). The first 17 proteins listed are either described as "Dab1 proteins" or "predicted: similar to Dab1 proteins". Furthermore, all of the first 16 proteins listed contain SEQ ID NO:3. Dab1 from Danio rerio, gi68440873, (number 17 on the list) is the first Dab1 protein listed that does not contain this 14 amino acid sequence, and it differs only in 1 amino acid (see Exhibit 6). Furthermore, other proteins listed such as mDab271, unnamed protein, Chain B, disabled homolog 2 isoform b, etc. do not share homology with SEQ ID NO:3.

While serine 491 of SEQ ID NO:4 falls within SEQ ID NO:3, serine 515 does not. Inclusion of SEQ ID NO:3 in the claim is independent of the positioning of "a serine corresponding to position 491 or 515 of SEQ ID NO:4". SEQ ID NO:3 was added to the claim to provide a structural reference to distinguish it from other materials.

Applicants provide as Exhibits 2 - 6 alignments of Homo sapiens, Canis familiaris, Gallus gallus, Bos taurus and Danio rerio Dab1 proteins with the Mus musculus Dab1 protein. Applicants show that a person of skill in the art using this amino acid sequence alignment can easily identify a serine from the Dab1 protein of any species that corresponds to serine 491 or 515 of murine Dab1.

However, in an attempt to further prosecution, Applicants have amended claim 1 to state that a phosphorylated serine at position 491 or 515 of SEQ ID NO:4 or SEQ ID NO:5 is indicative of Cdk5 serine kinase activity.

In view of the above arguments and amendments, all grounds for the rejection under 35 U.S.C. § 112, second paragraph have been obviated or overcome. Reconsideration and withdrawal of this rejection are respectfully requested.

35 U.S.C. § 112, First Paragraph

The Examiner rejected claims 1, 4-8, 10-11 and 13-15 under 35 USC 112, first paragraph, for failing to comply with the written description requirement. The Examiner rejected the claims for introducing new matter based on the addition of SEQ ID NO:3. The Examiner also maintained the previous scope of enablement rejection of Claims 1, 4-8, 10-11 and 13-15. The Examiner asserts that the claims are drawn to a method for detecting Cdk5 activity by determining whether a genus of Dab1 proteins is phosphorylated on a specific serine and that an invention involving a genus requires a precise definition, such as a structure, formula or chemical name of the claimed subject matter to sufficiently distinguish it from other materials.

Applicants disagree. SEQ ID NO: 3 is provided as a structural reference for the genus of Dab1 protein. A peptide having the sequence of SEQ ID NO:3 as shown in the specification was used as an antigen to generate an antibody that binds to Dab1. The use of this peptide as an antigen as described in the specification reveals to one of skill in the art that this is a sequence useful for distinguishing Dab1 from other proteins. Therefore, it is entirely appropriate for Applicants to use SEQ ID NO:3 in the claims for this purpose. Doing so does not introduce new matter into the specification.

However, in an effort to further prosecution, Applicants have amended Claim 1 to recite a serine phosphorylated at position 491 or 515 of SEQ ID NO:4 or SEQ ID NO:5 is

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indicative of Cdk5 serine kinase activity. Reference to SEQ ID NO:3 has been removed, rendering the new matter rejection moot.

Amendment of Claim 1 to recite a particular serine of SEQ ID NO:4 or SEQ ID NO:5 focuses the scope of the claims to that which is enabled by the teachings of the specification.
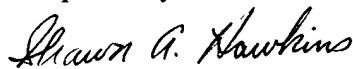
In view of the above arguments and amendments, all grounds for the rejections under 35 U.S.C. § 112, first paragraph have been obviated or overcome. Reconsideration and withdrawal of these rejections are respectfully requested.

Conclusion

It is believed that all the rejections have been obviated or overcome and the claims are in condition for allowance.

It is not believed that extensions of time or fees for net addition of claims are required. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR § 1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 501968.

Respectfully submitted,

Shawn A. Hawkins
Registration No. 50,318

	BLAST	Protein	Structure	PubMed	Taxonomy
NCBI	Genome	Nucleotide	3D-Domains	Books	Help

Query: gi|1771282 mDab555 protein [Mus musculus]
Matching gi: 70909361

| Show identical | Best hits | Common Tree | Taxonomy Report | 3D structures | CDD-Search | G |

199 BLAST hits to 23 unique species Sort by taxonomy proximity

| 0 | Archaea | 0 | Bacteria | 195 | Metazoa | 2 | Fungi | 0 | Plants | 0 | Viruses | 0 | Other Eukaryotae |
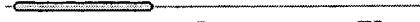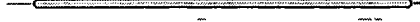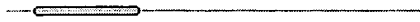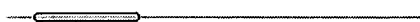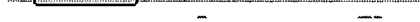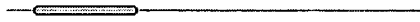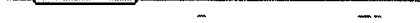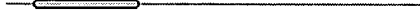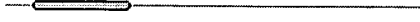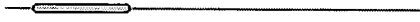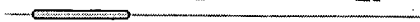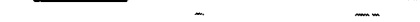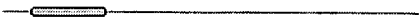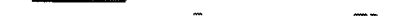
Keep only [▼] Cut-Off [100]   Select   New search by GI: [1771282]
Reset   Go

555 aa

SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
				Conserved Domain Database hits
2861	28	NP_705885	24025618	disabled homolog 1 [Rattus norvegicus]
2844	30	P97318	20137771	Disabled homolog 1
2805	22	BAE06094	68533079	DAB1 variant protein [Homo sapiens]
2805	22	CAI22361	56205777	disabled homolog 1 (Drosophila) [Homo sap
2797	22	O75553	20137706	Disabled homolog 1
2791	22	Q9BGX5	20137926	Disabled homolog 1
2766	22	AAF73058	8118615	disabled-1 [Homo sapiens]
2761	22	CAI22362	56205778	disabled homolog 1 (Drosophila) [Homo sap
2648	21	XP_852920	73956392	PREDICTED: similar to Disabled homolog 1
2620	18	AAP70754	37933763	disabled-1 late isoform [Gallus gallus]
2605	18	NP_989569	45383654	disabled homolog 1 [Gallus gallus]
2528	22	AAH67445	45768837	DAB1 protein [Homo sapiens]
2528	22	AAH67446	45768290	DAB1 protein [Homo sapiens]
2424	21	XP_582976	76613795	PREDICTED: similar to Disabled homolog 1
2361	18	AAP70753	37933750	disabled-1 early isoform [Gallus gallus]
1622	22	AAH67447	45767671	DAB1 protein [Homo sapiens]
1509	15	XP_686628	68440873	PREDICTED: similar to disabled homolog 1 .
1450	15	CAF91155	47207922	unnamed protein product [Tetraodon nigrov
1247	30	CAA69663	1771280	mDab271 protein [Mus musculus]
1233	15	CAF97616	47227987	unnamed protein product [Tetraodon nigrov
1014	30	NP_034144	6753596	disabled homolog 1 isoform 1 [Mus musculu
1014	22	CAI22363	56205779	disabled homolog 1 (Drosophila) [Homo sap
1011	30	AAH51993	30354111	Unknown (protein for MGC:62305) [Mus musc
993	22	CAI22360	56205776	disabled homolog 1 (Drosophila) [Homo sap
900	30	BAB24163	12838321	unnamed protein product [Mus musculus]
831	21	XP_868054	73953834	PREDICTED: similar to disabled homolog 2
814	30	1OQNB	34810824	Chain B, Crystal Structure Of The Phospho
812	30	BAE38389	74227265	unnamed protein product [Mus musculus]
809	28	AAC33406	3157995	DOC-2 p59 isoform [Rattus norvegicus]
807	30	NP_001...	83776585	disabled homolog 2 isoform b [Mus musculu
804	30	BAE38234	74225063	unnamed protein product [Mus musculus]
803	30	AAB02647	1176372	p67
800	30	AAH06588	13879242	Dab2 protein [Mus musculus]
797	17	AAH60027	37747715	MGC68686 protein [Xenopus laevis]
795	22	XP_513436	55587140	PREDICTED: complement component 8, beta p
794	22●	CAH89644	55725725	hypothetical protein [Pongo pygmaeus]
792	21	XP_586135	76646481	PREDICTED: similar to disabled homolog 2
776	30	1NU2A	30749751	Chain A, Crystal Structure Of The Murine
774	17	AAH59999	37748655	MGC68513 protein [Xenopus laevis]
768	30	BAE37047	74184017	unnamed protein product [Mus musculus]

745	15	AAH65585	41350978	Dab2 protein [Danio rerio]
741	15	NP_991320	45544644	disabled homolog 2 [Danio rerio]
590	30	BAB22405	12833137	unnamed protein product [Mus musculus]
590	21	XP_884109	76646479	PREDICTED: similar to Disabled homolog 2
590	30	AAB02646	1176371	p96
590	30	P98078	85681927	Disabled homolog 2 (DOC-2) (Mitogen-respo
590	30	AAG44669	12005916	disabled-2 p96 [Mus musculus]
590	30	A57542	2137622	p96 protein - mouse
590	30	NP_075607	83776557	disabled homolog 2 isoform a [Mus musculu
588	28	AAH97314	67677921	Disabled homolog 2 [Rattus norvegicus]
586	21	XP_868048	73953832	PREDICTED: similar to Disabled homolog 2
586	22	AAH03064	13111754	Disabled homolog 2 [Homo sapiens]
586	22	NP_001334	4503251	disabled homolog 2 [Homo sapiens]
586	21	XP_536493	73953830	PREDICTED: similar to Disabled homolog 2
584	22	AAB19032	1110539	mitogen-responsive phosphoprotein [Homo s
584	21	XP_871876	76646483	PREDICTED: similar to Disabled homolog 2
584	21	XP_884231	76646487	PREDICTED: similar to Disabled homolog 2
584	22	AAF23161	6671334	disabled-2 [Homo sapiens]
563	18	XP_425023	50762348	PREDICTED: similar to Disabled homolog 2
561	21	XP_868058	73953836	PREDICTED: similar to Disabled homolog 2
560	30	AAB02645	1176370	p93
558	21	XP_884203	76646485	PREDICTED: similar to Disabled homolog 2
554	15	XP_701354	68442893	PREDICTED: similar to disabled homolog 1,
552	22	XP_517792	55624400	PREDICTED: similar to disabled 2 p93 [Pan
552	22	AAF05540	6176336	disabled 2 p93 [Homo sapiens]
546	15	CAG05213	47228393	unnamed protein product [Tetraodon nigrov
537	21	AAI11685	84201636	Unknown (protein for IMAGE:8181047) [Bos
528	30	1P3RC	34810869	Chain C, Crystal Structure Of The Phospho
519	15	XP_692633	68361094	PREDICTED: similar to Disabled homolog 2
515	22	AAA93195	307331	differentially expressed protein
505	22	CAI22364	56205780	disabled homolog 1 (Drosophila) [Homo sap
505	22	XP_513437	55587142	PREDICTED: similar to DAB1 protein [Pan t
376	9	XP_797969	72149808	PREDICTED: similar to CG9695-PA [Strongyl
371	8	P98081	66774176	Protein disabled
371	8	EAL30332	54641582	GA21968-PA [Drosophila pseudoobscura]
371	8	AAB08527	1498252	disabled
369	8	XP_316563	58388821	ENSANGP00000004338 [Anopheles gambiae str
367	8	XP_624791	66516204	PREDICTED: similar to ENSANGP00000004338
328	7	CAE57702	39587234	Hypothetical protein CBG00708 [Caenorhabd
327	7	NP_495732	71992772	DAB (Drosophila disabled) homolog family
327	15	CAF95033	47210151	unnamed protein product [Tetraodon nigrov
322	7	NP_495730	71992767	DAB (Drosophila disabled) homolog family
322	7	NP_495731	71992758	DAB (Drosophila disabled) homolog family
322	7	A88230	25354045	protein M110.5 [imported] - Caenorhabditi
263	8	XP_557214	57919049	ENSANGP00000029543 [Anopheles gambiae str
247	15	AAH57504	34784107	Dab2 protein [Danio rerio]
245	28	AAC03361	2897137	mitogen-responsive phosphoprotein [Rattus
211	15	CAG13594	47203874	unnamed protein product [Tetraodon nigrov
200	21	XP_535996	74004972	PREDICTED: similar to GULP, engulfment ad
199	30	NP_082726	28201936	PTB domain adaptor protein CED-6 isoform
199	30	AAH32154	21618966	Gulp1 protein [Mus musculus]
199	30	NP_081782	21311823	PTB domain adaptor protein CED-6 isoform
196	18	XP_421848	50750045	PREDICTED: similar to GULP, engulfment ad
193	28	NP_001...	61557172	GULP, engulfment adaptor PTB domain conta
192	15	AAI07974	79158598	GULP, engulfment adaptor PTB domain conta
185	22	NP_057399	7705318	GULP, engulfment adaptor PTB domain conta
179	15	CAF98968	47220203	unnamed protein product [Tetraodon nigrov
176	21	XP_867869	73963539	PREDICTED: similar to numb homolog isofor
166	22	AAH01103	12654539	GULP1 protein [Homo sapiens]
166	18	NP_990166	45382287	numb homolog [Gallus gallus]
164	21	AAI09764	81674335	Unknown (protein for MGC:134569) [Bos tau
164	22	AAY24122	62988735	unknown [Homo sapiens]

163	22	AAH68476	46250416	Numb homolog, isoform 4 [Homo sapiens]
159	22	NP_001...	54144629	numb homolog isoform 4 [Homo sapiens]
157	22	CAH91534	55729610	hypothetical protein [Pongo pygmaeus]
157	28	NP_579821	82524268	numb gene homolog [Rattus norvegicus]
157	15	XP_693310	68366834	PREDICTED: similar to SI:bY36G15.1 (novel
154	22	NP_001...	54144627	numb homolog isoform 2 [Homo sapiens]
154	8	XP_392026	66523524	PREDICTED: similar to ENSANGP00000021640
153	28	ABC69735	85070124	numb isoform o/o [Rattus norvegicus]
152	30	AAB09586	1575756	m-Numb [Mus musculus]
151	22	AAD27959	4691549	NUMB protein [Homo sapiens]
151	21	XP_867877	73963541	PREDICTED: similar to numb homolog isofor
150	21	XP_867903	73963549	PREDICTED: similar to numb homolog isofor
150	21	XP_588484	76611402	PREDICTED: similar to low density lipopro
150	28	XP_220798	62656707	PREDICTED: similar to ubiquitin specific
150	30	AAH33459	23270973	Numb protein [Mus musculus]
150	30	BAB23367	12835800	unnamed protein product [Mus musculus]
148	22	Q5SW96	73921718	Low density lipoprotein receptor adapter
148	28	ABC69734	85070122	numb isoform i/o [Rattus norvegicus]
148	22	CAI16483	55962123	LDL receptor adaptor protein (ARH) [Homo
147	30	NP_035079	6754912	numb gene homolog [Mus musculus]
147	30	BAE35380	74204621	unnamed protein product [Mus musculus]
147	30	Q8C142	73921719	Low density lipoprotein receptor adapter
147	28	XP_575931	62649833	PREDICTED: similar to LDL receptor adapto
147	21	XP_867847	73963533	PREDICTED: similar to numb homolog isofor
147	30	BAC26238	26324968	unnamed protein product [Mus musculus]
146	17	CAJ81873	89273752	OTTXETP00000000331 [Xenopus tropicalis]
146	18	XP_417736	50759690	PREDICTED: similar to LDL receptor adapto
145	17	Q67FQ3	73921717	Low density lipoprotein receptor adapter
145	17	AAH68810	46250128	MGC81404 protein [Xenopus laevis]
145	21	XP_867889	73963545	PREDICTED: similar to numb homolog isofor
145	21	XP_855049	73950589	PREDICTED: similar to low density lipopro
145	17	Q801G1	73921716	Low density lipoprotein receptor adapter
143	15	XP_695452	68438641	PREDICTED: similar to GULP, engulfment ad
141	21	XP_885051	76641663	PREDICTED: similar to numb homolog (Droso
141	21	XP_885074	76641665	PREDICTED: similar to numb homolog (Droso
139	7	CAE64299	39584875	Hypothetical protein CBG08974 [Caenorhabd
138	22	BAB14908	10436776	unnamed protein product [Homo sapiens]
138	22	AAH29770	20987600	ARH protein [Homo sapiens]
138	30	NP_663529	21704092	low density lipoprotein receptor adaptor
137	22	CAD66588	28375609	unnamed protein product [Homo sapiens]
137	30	AAD47834	5713183	71 kDa Numb protein isoform [Mus musculus
137	21	XP_537504	73963551	PREDICTED: similar to numb homolog isofor
137	1	AAX36723	60825530	numb-like [synthetic construct]
137	21	XP_867842	73963531	PREDICTED: similar to numb homolog isofor
137	21	XP_867882	73963543	PREDICTED: similar to numb homolog isofor
137	22	AAH20788	18088523	NUMB protein [Homo sapiens]
137	28	ABC69736	85070126	numb isoform o/i [Rattus norvegicus]
136	15	AAI07954	79160060	Numb homolog [Danio rerio]
134	15	BAD89560	59275985	numb homolog [Danio rerio]
134	15	CAG09924	47219570	unnamed protein product [Tetraodon nigrov
133	30	1WJ1A	56966911	Chain A, Solution Structure Of Phosphotyr
133	15	CAI21213	56208059	novel protein containing a phosphotyrosin
133	15	NP_945331	39752651	hypothetical protein LOC368278 [Danio rer
132	22	CAD62362	28193240	unnamed protein product [Homo sapiens]
132	22	XP_510045	55641017	PREDICTED: similar to NUMB protein [Pan t
132	22	NP_001...	54144625	numb homolog isoform 1 [Homo sapiens]
132	30	Q9QZS3	14194994	Protein numb homolog (m-Numb) (m-Nb)
132	21	XP_867897	73963547	PREDICTED: similar to Numb protein homolo
132	28	ABC69737	85070128	numb isoform i/i [Rattus norvegicus]
131	7	AAW26009	56755661	SJCHGC02254 protein [Schistosoma japonicu
131	17	AAI06374	76780336	Unknown (protein for MGC:130936) [Xenopus
129	30	BAE27971	74184738	unnamed protein product [Mus musculus]
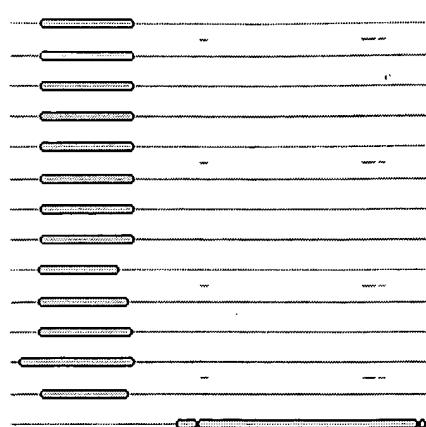
129	28	NP_001...	76559905	numb-like [Rattus norvegicus]
129	1	AAX32221	60655315	numb-like [synthetic construct]
129	21	XP_855314	73948318	PREDICTED: similar to numb homolog (Droso
129	22	Q9Y6R0	14194976	Numb-like protein (Numb-R)
129	30	O08919	51704231	Numb-like protein
129	30	NP_035080	87042277	numb-like [Mus musculus]
129	30	AAB58697	2149943	Numblike [Mus musculus]
128	15	CAG06441	47224871	unnamed protein product [Tetraodon nigrov
128	22	XP_524622	55586633	PREDICTED: hypothetical protein XP_524622
128	15	CAG09113	47224267	unnamed protein product [Tetraodon nigrov
126	8	EAL26939	54637537	GA18153-PA [Drosophila pseudoobscura]
126	7	AAX24514	76152838	SJCHGC02255 protein [Schistosoma japonicu
125	22	CAH91693	55729933	hypothetical protein [Pongo pygmaeus]
124	4	NP_982814	45185097	ABL133Cp [Eremothecium gossypii]

Exhibit 2

Blast 2 Sequences results

NCBI

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix [BLOSUM62 ▼] gap open: [11] gap extension: [1]
x_dropoff: [50] expect: [300.00] wordsize: [3] Filter □ View option [Standard ▼]
Masking character option [X for protein, n for nucleotide ▼] Masking color option [Black ▼]
□ Show CDS translation [Align]

Sequence 1: gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]
Length = 555 (1 .. 555)

Sequence 2: gi|68533079|dbj|BAE06094.1|DAB1 variant protein [Homo sapiens]
Length = 559 (1 .. 559)
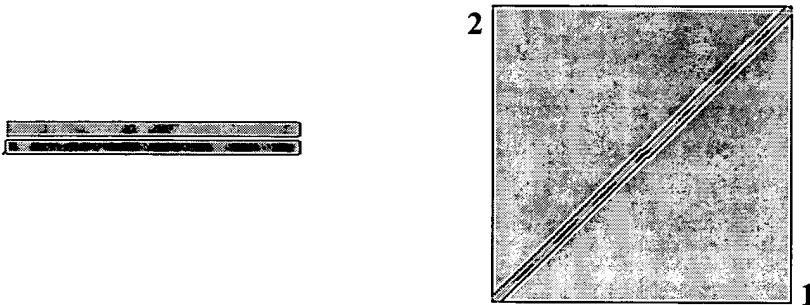
NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score = 1085 bits (2805),  Expect = 0.0
 Identities = 536/555 (96%),  Positives = 543/555 (97%),  Gaps = 0/555 (0%)

Query    1    MSTETELQVAVKTSAKKDSRKKGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKL    60
              MSTETELQVAVKTSAKKDSRKKGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKL
Sbjct    5    MSTETELQVAVKTSAKKDSRKKGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKL    64

Query   61    CQDSMMKLKGVVAGARSKGEHKQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDI   120
              CQDSMMKLKGVVAGARSKGEHKQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDI
Sbjct   65    CQDSMMKLKGVVAGARSKGEHKQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDI   124

Query  121    TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQC   180
              TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQC
Sbjct  125    TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQC   184

Query  181    EQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPV   240
              EQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPV
Sbjct  185    EQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPV   244

Query  241    SAVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSSQTLPGSADVFGSMSFGTAAVPSGY   300
              SAVTQLELFGDMSTPPDITSPPTPATPGDAF+PSSSQTLP SADVF S+ FGTAAVPSGY
```

```
Sbjct  245  SAVTQLELFGDMSTPPDITSPPTPATPGDAFIPSSSQTLPASADVFSSVPFGTAAVPSGY  304

Query  301  VAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVIPGAQPIAWGQPGLFPATQQAWPTVAGQ  360
            VAMGAVLPSFWGQQPLVQQQ+ MGAQPPVAQV+PGAQPIAWGQPGLFPATQQ WPTVAGQ
Sbjct  305  VAMGAVLPSFWGQQPLVQQQMVMGAQPPVAQVMPGAQPIAWGQPGLFPATQQPWPTVAGQ  364

Query  361  FPPAAFMPTQTVMPLAAAMFQGPLTPLATVPGTNDSARSSPQSDKPRQKMGKESFKDFQM  420
            FPPAAFMPTQTVMPL AAMFQGPLTPLATVPGT+DS RSSPQ+DKPRQKMGKE+FKDFQM
Sbjct  365  FPPAAFMPTQTVMPLPAAMFQGPLTPLATVPGTSDSTRSSPQTDKPRQKMGKETFKDFQM  424

Query  421  VQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTN  480
             QPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTN
Sbjct  425  AQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTN  484
```

          491   515

```
Query  481  SPPTPAPRQSSPSKSSASHVSDPTADDIFEEGFESPSKSEEQEAPDGSQASSTSDPFGEP  540
            SPPTPAPRQSSPSKSSASH SDPT DDIFEEGFESPSKSEEQEAPDGSQASS SDPFGEP
Sbjct  485  SPPTPAPRQSSPSKSSASHASDPTTDDIFEEGFESPSKSEEQEAPDGSQASSNSDPFGEP  544
```

SEQ ID NO:3 —1

```
Query  541  SGEPSGDNISPQDGS  555
            SGEPSGDNISPQ GS
Sbjct  545  SGEPSGDNISPQAGS  559
```

```
CPU time:      0.05 user secs.        0.02 sys. secs        0.07 total secs.

Lambda      K        H
  0.311     0.129     0.373


Gapped
Lambda      K        H
  0.267     0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3330
Number of extensions: 1692
Number of successful extensions: 10
Number of sequences better than 300.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 555
Length of database: 1,196,146,007
Length adjustment: 138
Effective length of query: 417
Effective length of database: 1,196,145,869
Effective search space: 498792827373
Effective search space used: 498792827373
Neighboring words threshold: 9
X1: 16 ( 7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.8 bits)
S2: 68 (30.8 bits)
```

Blast 2 Sequences results

NCBI

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix BLOSUM62 ▾ gap open: 11 gap extension: 1
x_dropoff: 50 expect: 300.00 wordsize: 3 Filter ☐ View option Standard ▾
Masking character option X for protein, n for nucleotide ▾ Masking color option Black ▾
☐ Show CDS translation Align

Sequence 1: gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]
Length = 555 (1 .. 555)

Sequence 2: gi|73956392|ref|XP_852920.1|PREDICTED: similar to Disabled homolog 1 [Canis familiaris]
Length = 678 (1 .. 678)
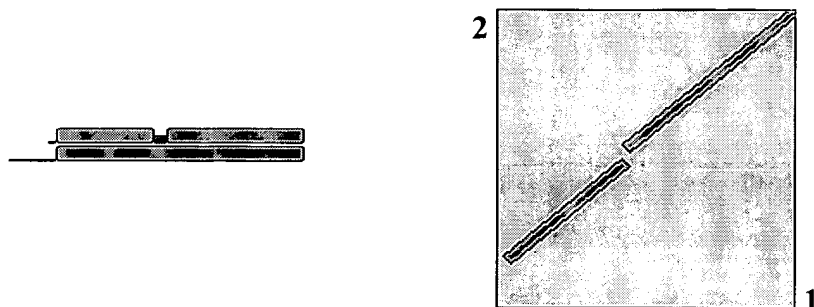
NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score = 1024 bits (2648),  Expect = 0.0
 Identities = 513/567 (90%), Positives = 520/567 (91%), Gaps = 33/567 (5%)

Query  22   KGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH   81
            +GQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH
Sbjct  112  QGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH  171

Query  82   KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI  141
            KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI
Sbjct  172  KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI  231

Query  142  KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYI  201
            KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYI
Sbjct  232  KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYI  291

Query  202  VFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPVS-------------------  241
            VFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPVS
Sbjct  292  VFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPVSNGQPFEDFEERFAAATPNRN  351

Query  242  -------------AVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSSQTLPGSADVFGS  288
                         AVTQLELFGDMSTPPDITSPPTPATPGDAF+PSSSQTLP SAD+F S
```

```
Sbjct  352  LPMDFDEILEATKAVTQLELFGDMSTPPDITSPPTPATPGDAFIPSSSQTLPASADMFSS  411

Query  289  MSFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVIPGAQPIAWGQPGLFP  348
            + FGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQV+PGAQPIAWGQPGLFP
Sbjct  412  VPFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVMPGAQPIAWGQPGLFP  471

Query  349  ATQQAWPTVAGQFPPAAFMPTQTVMPLAAAMFQGPLTPLATVPGTNDSARSSPQSDKPRQ  408
            ATQQ WPTVAGQFPPAAFMPTQTVMPL AAMFQGPLTPLATVP T DS RSSPQ++KPRQ
Sbjct  472  ATQQPWPTVAGQFPPAAFMPTQTVMPLPAAMFQGPLTPLATVPTTGDSTRSSPQTEKPRQ  531

Query  409  KMGKESFKDFQMVQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN  468
            KMGKE FKDFQM QPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN
Sbjct  532  KMGKEMFKDFQMAQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN  591

Query  469  LTPVTSTTPSTNSPPTPAPRQSSPSKSSASHVSDPTADDIFEEGFESPSKSEEQEAPDGS  528
            LTPVTSTTPSTNSPP TPAPRQSSPSKSSASH SDPT DDIFEEGFESPSKSEEQEAPDGS
Sbjct  592  LTPVTSTTPSTNSPPTPAPRQSSPSKSSASHASDPTTDDIFEEGFESPSKSEEQEAPDGS  651

Query  529  QASSTSDPFGEPSGEPSGDNISPQDGS  555
            QASS SDPFGEPSGEPSGDNISPQ GS
Sbjct  652  QASSNSDPFGEPSGEPSGDNISPQAGS  678
```

491 ... 515

1 — SEQ ID NO.3 — 1

```
CPU time:      0.05 user secs.        0.01 sys. secs        0.06 total secs.

Lambda       K        H
   0.311     0.129     0.373

Gapped
Lambda       K        H
   0.267     0.0410      0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3685
Number of extensions: 1958
Number of successful extensions: 11
Number of sequences better than 300.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 555
Length of database: 1,196,146,007
Length adjustment: 138
Effective length of query: 417
Effective length of database: 1,196,145,869
Effective search space: 498792827373
Effective search space used: 498792827373
Neighboring words threshold: 9
X1: 16 ( 7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.8 bits)
S2: 68 (30.8 bits)
```

Exhibit 4

Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix [BLOSUM62 ▾] gap open: [11] gap extension: [1]
x_dropoff: [50] expect: [300.00] wordsize: [3] Filter ☐ View option [Standard ▾]
Masking character option [X for protein, n for nucleotide ▾] Masking color option [Black ▾]
☐ Show CDS translation [Align]

Sequence 1: gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]
Length = 555 (1 .. 555)

Sequence 2: gi|37933763|gb|AAP70754.1|disabled-1 late isoform [Gallus gallus]
Length = 551 (1 .. 551)
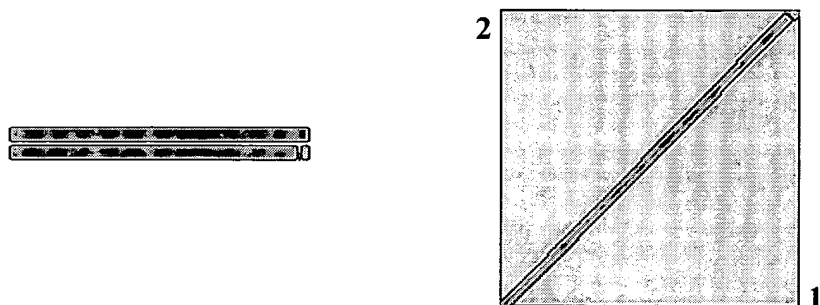
NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score = 1013 bits (2620),  Expect = 0.0
 Identities = 497/555 (89%), Positives = 523/555 (94%), Gaps = 4/555 (0%)

Query  1    MSTETELQVAVKTSAKKDSRKKGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKL  60
            MSTETELQVAVKTS KKDS+KKGQDRSEATLIKRFKG+GVRYKAKLIGIDEVSAARGDKL
Sbjct  1    MSTETELQVAVKTSTKKDSKKKGQDRSEATLIKRFKGDGVRYKAKLIGIDEVSAARGDKL  60

Query  61   CQDSMMKLKGVVAGARSKGEHKQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDI  120
            CQDSMMKLKG+VA ARSKGEHKQKIFLT+SFGGIKIFDEKTG LQHHHAVHEISYIAKDI
Sbjct  61   CQDSMMKLKGIVAAARSKGEHKQKIFLTVSFGGIKIFDEKTGLLQHHHAVHEISYIAKDI  120

Query  121  TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQC  180
            TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREE+EKKAQKDKQC
Sbjct  121  TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREEMEKKAQKDKQC  180

Query  181  EQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPV  240
            EQAVYQTILEEDVEDPVYQYIVFEAGHEPIR+PETEENIYQVPTSQKKEGVYDVPKSQPV
Sbjct  181  EQAVYQTILEEDVEDPVYQYIVFEAGHEPIREPETEENIYQVPTSQKKEGVYDVPKSQPV  240

Query  241  SAVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSSQTLPGSADVFGSMSFGTAAVPSGY  300
            SAVTQLELFGDMSTPPD+TSPPTPATPGDAF+PSSSQ+LP S D+FGS+ F TAAVPSGY
```

```
Sbjct  241   SAVTQLELFGDMSTPPDVTSPPTPATPGDAFIPSSSQSLPASTDMFGSVPFSTAAVPSGY   300

Query  301   VAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVIPGAQPIAWGQPGLFPATQQAWPTVAGQ   360
             VAMGAVLPSFWGQQPLVQQQ+AMGAQPPVAQV+ G QPIAWGQPG+FP   QQ WP+VAGQ
Sbjct  301   VAMGAVLPSFWGQQPLVQQQLAMGAQPPVAQVMQGGQPIAWGQPGIFPPAQQPWPSVAGQ   360

Query  361   FPPAAFMPTQTVMPLAAAMFQGPLTPLATVPGTNDSARSSPQSDKPRQKMGKESFKDFQM   420
             F P AFMPTQTV+PL AAMFQG + P+ATVP T+DS RSSPQ+D+PRQKMGKE FKDFQM
Sbjct  361   FQPTAFMPTQTVLPLQAAMFQGTIAPIATVPPTSDSNRSSPQTDRPRQKMGKEMFKDFQM   420

Query  421   VQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTN   480
              QPPPVPSRKPDQPSL+CTSEAFSSYFNKVG+AQ+ DDCDDFDISQLNLTPVTSTTPSTN
Sbjct  421   AQPPPVPSRKPDQPSLSCTSEAFSSYFNKVGMAQEADDCDDFDISQLNLTPVTSTTPSTN   480

Query  481   SPPTPAPRQSSPSKSSASHVSDPTADDIFEEGFESPSKSEEQEAPDGSQASSTSDPFGEP   540
             SPPTPAPRQSSPSKSSASH SDP ADD+FEEGFESPSKSEEQEAPD SQASS SDPF
Sbjct  481   SPPTPAPRQSSPSKSSASHTSDPAADDLFEEGFESPSKSEEQEAPDESQASSNSDPF---   537

Query  541   SGEPSGDNISPQDGS   555
             GEP+GD ISPQ GS
Sbjct  538   -GEPTGDTISPQVGS   551
```

```
CPU time:      0.05 user secs.        0.01 sys. secs        0.06 total secs.

Lambda     K        H
  0.311    0.129    0.373

Gapped
Lambda     K        H
  0.267    0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3243
Number of extensions: 1668
Number of successful extensions: 10
Number of sequences better than 300.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 555
Length of database: 1,196,146,007
Length adjustment: 138
Effective length of query: 417
Effective length of database: 1,196,145,869
Effective search space: 498792827373
Effective search space used: 498792827373
Neighboring words threshold: 9
X1: 16 ( 7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.8 bits)
S2: 68 (30.8 bits)
```

NCBI · **Blast 2 Sequences results**

**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]**

Matrix [BLOSUM62 ▼] gap open: [11] gap extension: [1]
x_dropoff: [50] expect: [300.00] wordsize: [3] Filter ☐ View option [Standard ▼]
Masking character option [X for protein, n for nucleotide ▼] Masking color option [Black ▼]
☐ Show CDS translation [Align]

Sequence 1: gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]
Length = 555 (1 .. 555)

Sequence 2: gi|76613795|ref|XP_582976.2|PREDICTED: similar to Disabled homolog 1 [Bos taurus]
Length = 542 (1 .. 542)
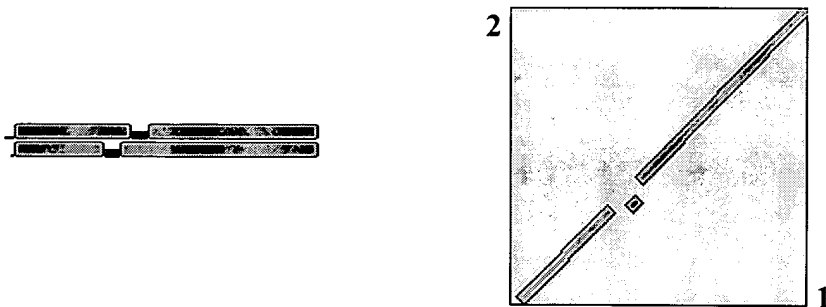
NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score =  938 bits (2424),  Expect = 0.0
 Identities = 480/567 (84%), Positives = 485/567 (85%), Gaps = 68/567 (11%)

Query   22   KGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH   81
             KGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH
Sbjct   11   KGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH   70

Query   82   KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI   141
             KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI
Sbjct   71   KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI   130

Query   142  KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYI   201
             KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQ
Sbjct   131  KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQ---------------  175

Query   202  VFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPVS-------------------  241
                                 VPTSQKKEGVYDVPKSQPVS
Sbjct   176  -------------------VPTSQKKEGVYDVPKSQPVSNGRAFEDFDERFAAATPNRN   215

Query   242  -------------AVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSSQTLPGSADVFGS   288
                          AVTQLELFGDMSTPPDITSPPTPATPGDAF+PSSSQTLP SADV GS
```

```
Sbjct   216  LPMDFDEIFEATKAVTQLELFGDMSTPPDITSPPTPATPGDAFIPSSSQTLPASADVCGS   275

Query   289  MSFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVIPGAQPIAWGQPGLFP   348
             +  FGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQV+PGAQPIAWGQPGLFP
Sbjct   276  LPFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVMPGAQPIAWGQPGLFP   335

Query   349  ATQQAWPTVAGQFPPAAFMPTQTVMPLAAAMFQGPLTPLATVPGTNDSARSSPQSDKPRQ   408
             A QQ WP VAGQFPPAAFMPTQTVMPL AAMFQGPLTPLAT+P T DSARSSPQ+DKPRQ
Sbjct   336  AAQQPWPAVAGQFPPAAFMPTQTVMPLPAAMFQGPLTPLATIPATGDSARSSPQTDKPRQ   395

Query   409  KMGKESFKDFQMVQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN   468
             KMGKE FKDFQM QPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN
Sbjct   396  KMGKEMFKDFQMAQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN   455
                                491                          95
Query   469  LTPVTSTTPSTNSPPTPAPRQSSPSKSSASHVSDPTADDIFEEGFESPSKSEEQEAPDGS   528
             LTPVTSTTPSTNSPPTPAPRQSSPSKSSASH SDPTADDIFEEGFESPSKSEEQEAPDGS
Sbjct   456  LTPVTSTTPSTNSPPTPAPRQSSPSKSSASHASDPTADDIFEEGFESPSKSEEQEAPDGS   515
                              1— SEQ ID NO:3 —1
Query   529  QASSTSDPFGEPSGEPSGDNISPQDGS   555
             QASS SDPFGEPSGEPSGDNISPQ GS
Sbjct   516  QASSNSDPFGEPSGEPSGDNISPQAGS   542
```

```
CPU time:      0.04 user secs.        0.01 sys. secs        0.05 total secs.

Lambda      K       H
   0.311    0.129    0.373

Gapped
Lambda      K       H
   0.267    0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3195
Number of extensions: 1648
Number of successful extensions: 13
Number of sequences better than 300.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 555
Length of database: 1,196,146,007
Length adjustment: 138
Effective length of query: 417
Effective length of database: 1,196,145,869
Effective search space: 498792827373
Effective search space used: 498792827373
Neighboring words threshold: 9
X1: 16 ( 7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.8 bits)
S2: 68 (30.8 bits)
```

Blast 2 Sequences results

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix [BLOSUM62 ▼] gap open: [11] gap extension: [1]

x_dropoff: [50] expect: [300.00] wordsize: [3] Filter ☐ View option [Standard ▼]

Masking character option [X for protein, n for nucleotide ▼] Masking color option [Black ▼]

☐ Show CDS translation [Align]

Sequence 1: gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]
Length = 555 (1 .. 555)

Sequence 2: gi|68440873|ref|XP_686628.1|PREDICTED: similar to disabled homolog 1 [Danio rerio]
Length = 487 (1 .. 487)
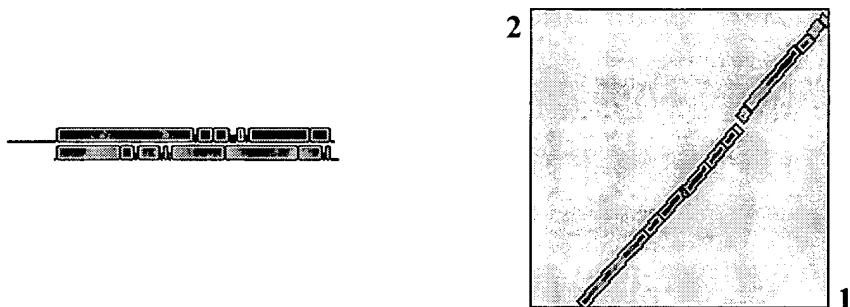
NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score =  585 bits (1509),  Expect = 2e-165
 Identities = 318/478 (66%), Positives = 359/478 (75%), Gaps = 34/478 (7%)

Query  97   FDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRD  156
            F  + LQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAIKTAQ+AEPVILDLRD
Sbjct  8    FRRDSEVLQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAIKTAQSAEPVILDLRD  67

Query  157  LFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETE  216
            LFQLIYE+KQREE+EKKAQKDKQCEQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDP +E
Sbjct  68   LFQLIYEIKQREEIEKKAQKDKQCEQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDP-SE  126

Query  217  ENIYQVPTSQKKEGVYDVPKSQPVSAVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSS  276
            E+IYQVPTSQ+KEGVYDVPK  P   + QLELFGDMSTPPDITSP TPA+P +    P  +
Sbjct  127  ESIYQVPTSQQKEGVYDVPKRHP--NINQLELFGDMSTPPDITSPSTPASPANTLDPLLA  184

Query  277  QTLPGSADVFGSMSFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPP--VAQVIP  334
                P  +++F    F  A+VPSGYV MGAV P++  QQ   Q  +A G Q P  VAQV+P
Sbjct  185  HQTP--SELF--TPFNPASVPSGYVTMGAVPPAWAQQQFAAQAPLAFGVQSPVQVAQVLP  240

Query  335  GAQPIAWGQPGLFPATQQAWPTVAG-QFPPAAFMPTQTVMPLAAAMFQGPLTPLA-----  388
            G QP+ WGQ  LFPATQQ W  +AG  F PAAFMP QTV PL AAMFQ   L P+A
```

```
Sbjct   241   GTQPLIWGQANLFPATQQQWAAMAGAHFSPAAFMPAQTVGPLPAAMFQ-TLAPMAVPASC   299

Query   389   ---------TVPGTNDSARSSPQSD----KPRQKMGKESFKDFQMVQPPPVPSRKPDQPS   435
                       V GT+ S  SSPQ      + + KM KE FK+FQM +PP +P+RK +QPS
Sbjct   300   ETPTAAMGGAVAGTSASTASSPQHGERTLQRQAKMSKEMFKEFQMAKPPAMPARKGEQPS   359

Query   436   LTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTNSPPTPAPRQSSPSKS   495
              L+CT++AFSSYF++VG+AQDTDDCDDFDISQ+NLTPVTSTTPSTNSPPTPAPRQSSPSKS
Sbjct   360   LSCTTDAFSSYFSRVGMAQDTDDCDDFDISQMNLTPVTSTTPSTNSPPTPAPRQSSPSKS   419
                                                             I — SEQ ID NO.3

Query   496   SASHVSDPTADDIFEEGFESPSKS-EEQEAPDGSQASSTSDPFGEPSGEPSGDNISPQ   552
              S SH SDP  DD F E   SPS+S EE  A D  Q+   S+P  EP    S +   SPQ
Sbjct   420   S-SHASDPPTDDSFGEAEGSPSRSGEEDAAGDCPQSPGASEPQAEPE---SSETDSPQ   473
```

CPU time: 0.05 user secs.   0.01 sys. secs   0.06 total secs.

Lambda   K   H
  0.311   0.129   0.373

Gapped
Lambda   K   H
  0.267   0.0410   0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 2847
Number of extensions: 1507
Number of successful extensions: 18
Number of sequences better than 300.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 555
Length of database: 1,196,146,007
Length adjustment: 138
Effective length of query: 417
Effective length of database: 1,196,145,869
Effective search space: 498792827373
Effective search space used: 498792827373
Neighboring words threshold: 9
X1: 16 (7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (21.8 bits)
S2: 68 (30.8 bits)